130 140 150 160 1093 GGGGAAACCCAGCACGAGTGATGTCGTGTTACCCGCATCT M.tuberce 422 GGGGAACCCAGCACGAGTGATGTCGTGTTACCCGTATCT M.avium 422 GGGGAACCCAGCACGAGTGATGTCGTGTTACCCGTATCT M.paratu 507 GGGGAACCCAGCACGAGTGATGTCGTGTTACCCGTATCT M.phlei 432 GGGGAACCCAACGACGAGTGATGTCGTGTTACCCGTATCT M.leprace 207 GGGGAAACCCAGCACGAGTAATGTCGTGTTACCCGTATCT M.gastri 150 GGGGAAACCCAGCACGAGTGATGTCGTGTTACCCGCATCT M.kansai 2588 GGGGAAACCCGGCACGAGTGATGTCGTGTTACCCGCATCT M.smegm	uberc. e i sii
--	-------------------------

210 220 230 240 1172 CATCTCAGTACCCGTAGGAGGAGAAACAATTGTGATTCC M.tuberculosis 501 CATCTCAGTACCCGTAGGAGAAGAAACAATTGTGATTCC M.avium 501 CATCTCAGTACCCGTAGGAGAAGAAACAATTGTGATTCC M.paratuberc. 586 CATCTCAGTACCCGTAGGAGAAGAAACAATTGTGATTCC M.phlei 511 CATCTCAGTACCCGTAGGAGAAGAAACAATTGTGATTCC M.leprae 286 CATCTCAGTACCCGTAGGAGAAGAAACAAAAGTGATTCC M.gastri 229 CATCTCAGTACCCGTAGGAGAAGAAACAAAAGTGATTCC M.kansasii 220 CATCTCAGTGCCCGTAGGAAGAAAACAAAAGTGATTCC M.smegmatis						
CATCTCAGTACCCGTAGGAGAAAACAATTGTGATTCC M.paratuberc. CATCTCAGTACCCGTAGGAGAAGAAACAATTGTGATTCC M.phlei CATCTCAGTACCCGTAGGAGAAGAAAACAATTGTGATTCC M.leprae CATCTCAGTACCCGTAGGAGAAAACAATTGTGATTCC M.gastri CATCTCAGTACCCGTAGGAGAAAACAAAAGTGATTCC M.gastri		210	220			
	501 501 586 511 286	CATCTCAGTACCCGT CATCTCAGTACCCGT CATCTCAGTACCCGT CATCTCAGTACCCGT CATCTCAGTACCCGT	aggagaaa aggagaga aggagaga aggagaaga aggagaaga	AACAATTGTG AAACAATTGTG AAACAATTGTG AAACAATTGTG	SATTCC SATTCC SATTCC	M.paratuberc. M.phlei M.leprae M.gastri M.kansasii

				•	
	330	340	350	360	
		TOTAL CCCC	TACCCGGCTGAG	GA-GG M.tuberculos	is
1289	TGTGGGAG-GATATG	CTCAGCGC	TACCCCCCTGA(GA-GG M.tuberculos	
703					
629					
404					
	TGTGGGATGGATACG	TCTCAGCIIC	TACCCGGCTGA	GG-GG M.kansasii	
347	TGTGGGATOGATAGO		TACCHGGCTG	GAGGG M.smegmatis	
2785	TGTGGGACCTATUTE	LCCCGCGCEC	/1/10 o la la		

Figure 1A

				
	370	380	390	400
TAGTCAC TAGTCAC TAGTGAC TAGTCAC CAGTCAC	SAAAGTGTC SAAAGTGTC JAAAAGCAGT CAAAGTGTC GAAAGTGTC	ergettages etgettages etgettages etgettaacs	GAAGTGGCCT GAAGTGGCCT GGAAGTGGCCT GGAAGTGGCCT	GGGAT M.phlei
				
		4.50	470	 480
	450	460		CGGGCC M.tuberculosis
5 CGGCAGO TGCTG 7 TGGCAGO CGGCAGO	CCTGCCTIA CCTGCCTTG CCTGCCTTG CCTGCCTTG	TATCAACACC ACAGGTCC TATCAATTCC TATCAATTCC	CGAGTAGCAGCCGAGTAGCAGCCGAGTAGCAGCCGAGTAGCAGCCAGC	CGGGCC M.avium CGGGCC M.paratuberc. CGGGCC M.phlei CGGGCC M.leprae CGGGCC M.gastri CGGGCC M.kansasii CGGGCC M.smegmatis
		500	510	 520
	490	- 500	510	520 CGGTAAG M.tuberculosi CGGTAAG M.avium

Figure 1B

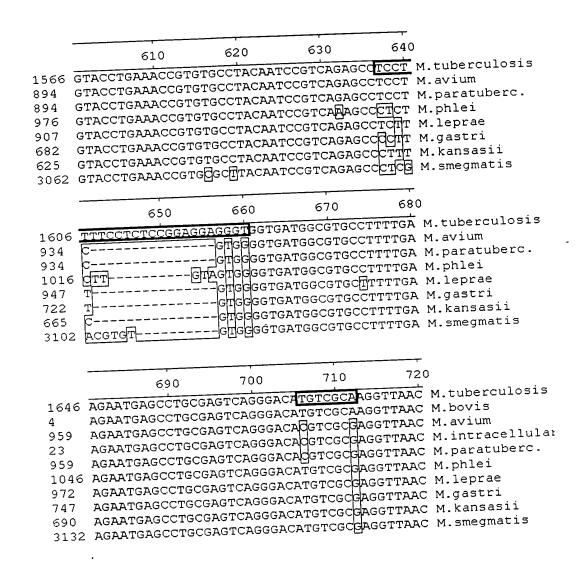


Figure 1C

					
	770	780	790	800	
TO C CONCC		TACGCGCGTG	rgaa ragtgo	GCGTGT M.tuberculosis	5
726 CGACC	CACACGCGCA	TACGCGCGTG			
039 CGF	cafrdcdcff	TTGGGGTGT	AGTG	GCGTGT M.avium GCGTGT M.intracellula	ar
03 CG	cardodor	TIGGGGIGT	n cric	GCGTGT M.paratuberc.	
1020 CG	CATCCTT	TITGGGGTGT	- 1	GTGTGT M.phlei	
		GGGGTTGGTG	AGTG	GCGTGT M.leprae	
1052 CGTAT	1	AGCGTGTGT- AGCGTGTGT	bgtg	GCGTGT M.gastri	
827 CGTAT	1-0	AGCGTGTGT	\ncTG	GCGTGT M.kansasıl	
770 CGTAT		GAGTGTGTG	TGTAGTG	GTGTGT M.smegmatis	
3212 CGTAT	<u> </u>				
		980	990	1000	
	970	980	an edebega	GTAGAG M.tuberculos	S
1926 ATTT	AGGTGCAGCG	TTGCGTGGTT	CACCIO DOSA.	GGTAGAG M.tuberculosi GGTAGAG M.avium GGTAGAG M.paratuberc	
1228 ATTT	AGGTGCAGCG	1160610011	achlecen	campang M. paratuberc	•
1228 ATTT	AGGTGCAGCG	rGcArcATT	CTTATCGGA	GGTAGAG M.phlei GGTAGAG M.leprae	
1322 ATT	'AGGIGCAGCG	TTGCGTGGTT	CACCACGGA	GGTAGAG M.leprae GGTAGAG M.gastri	
1010 ATTT	AGGTGCAGCG	TTGCGTGNTI	CACCACGGA	GGTAGAG M.gastri GGTAGAG M.kansasii	
962 ATT	TAGGTGCAGC	TTGCGTGTTT	CACCACGGA	GGTAGAG M.kansasii	
3408 ATT	raggtgcagc(et[GCF]TG[[T]	Clifedcage	GGTAGAG M.smegmatis	
		_			
			1070	1080	
	1050	1060	1070		≈i.
2005 CAG	CCAAACTCCG	AATGCCG-TG	GTG-TA-AA	GCGTGGCA M.tuberculog	
1307 CAG	CCAAACTCCG	AAIGOOG 10		CCCTCCCA M. paratuper	c.
1307 CAG	CCAAACTCC	AATGCCG	= = = = = = = = = = = = = = = = = = = =	cMcTGGCA M.phlei	
1401 CAG	CCAAACTCCC	AMIGCOGETE	TOTAL MANAGE	CCGTGGCA M.leprae	
1323 CA	3CCAAACTCC	JAMIGCOO 19		CCGTGGCA M.qastri	
1098 CAC		SAATGCCG-TO	GTG-TATA	GCGTGGCA M.kansasii AGTGCGGAA M.smegmatis	
1041 CA	CCAAACTCC CCCDDACTCC	GAATGCCGGT	AAGGCCAAG	AG[]GGGGA M.smegmatis	,
3480 CA	GOOMAGIOIO	<u> </u>			

Figure 1D

1130	1140	1150	1160
2082 ACAGCCCAGATCGCCC 1385 ACAGCCCAGATCGCCC 1385 ACAGCCCAGATCGCCC 1479 ACAGCCCAGATCGCCC 1401 ACAGCCCAGATCGCCC 1118 ACAGCCCAGATCGCCC 3566 ACAGCCCAGATCGCCC	GGCTAAGGCCC GGCTAAGGCCC GGCTAAGGCCC GGCTAAGGCCC	CTAAGCGTG CTAAGCGTG CTAAGCGTG CCAAAGCGTG	TGCTA M.paratuberc. TGCTA M.phlei TGCTA M.leprae TGCTA M.gastri
			
1290	1300	1310	1320
2241 CTCAAGCACACCGCC 1544 CTCAAGCACACCGCCC 1544 CTCAAGCACACCGCCCCCCCCCCCCCCCCCCCCCCCCCC	CGAAGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	GCACATICAT GCAF-ATCAG GCACATICAC ACAFAC	COTITG M.phlei CTTCTA M.leprae CGC-A M.gastri CGC-A M.kansasii
1583 GGTGGATGTGGGT 1583 GGTGGATGTGGGT 1676 TGGCTGGTGTGGGT 1600 GGGTGGATGTGGGT	ragggaagce raggggagce' raggggagce' raggggagce'	CCCCATTC CCTGCATCC CCTCATTC CCCTCATTC	1360 AGCGAAG M.tuberculosis AGCGAAG M.avium AGCGAAG M.paratuberc. GGTGAAG M.phlei AGCGAAG M.leprae AGCGAAG M.gastri AGCGAAG M.kansasii GGTGAAG M.smegmatis

Figure 1E

				
	1370	1380	1390	1400
1623 CT-CCGGG 1623 CT-CCGGG 1716 CCGCCGAG 1640 CCTCCGGG 1402 CCGCCGGG	TGACCGGTG TGATCGGTG TGATCGGTG TGACCGGTG	GTGGAGGGI GTGGAGGGI GTGGAGGGG GTGGAGGAGGA	GGGGGAGTG GGGGGAGTG GGGGGAGTG GGGGGAGTG	AGAAT M.tuberculosis AGAAT M.avium AGAAT M.paratuberc. AGAAT M.phlei AGAAT M.leprae AGAAT M.gastri AGAAT M.kansasii AGAAT M.smegmatis
	1410	1420	1430	1440
1662 GCAGGCA 1662 GCAGGCA 1756 GCAGGCA 1680 GCAGGCA 1442 GCAGGCA	TGAGTAGCG. TGAGTAGCG. TGAGTAGCG. TGAGTAGCG.	ATTAAGGCAA ATTAAGGCAA ATTAAGGCAA ATTAAGGCAA	GTGAGAACCT GTGAGAACCT GTGAGAACCT GTGAGAACCT	TTGCCC M.tuberculosis TTGCCC M.avium TTGCCC M.paratuberc. TTGCCC M.phlei TTGCCC M.leprae TTGCCC M.gastri TTGCCC M.kansasii TTGCCC M.smegmatis
			. 	
_	1570	1580	1590	1600
1821 CGMCCC 1821 CGMCCC 1915 CGMCCC 1840 CGCCCC 1602 CGCCCC	TGATGAATC TGATGAATC TGATGAATC TGATGAATC TGATGAATC	A-GCGGTAC A-GCGGTAC TCATTCTGC A-GCGGTAC A-GCGGTAC	TAACCACCCA TAACCACCCA TGACCACCCA TAACCACCCA	AAACCG M.tuberculosis AAACCG M.avium AAACCG M.paratuberc. AAACCM M.phlei AAACCG M.leprae AAACCG M.gastri AAAACCG M.kansasii AAACCA M.smegmatis

Figure 1F

				
_	1610	1620	1630	1640
1860 G 1860 G 1955 G 1879 G 1641 G	AT-CGACCAII-TCCCC AT-CGACCAII-TCCCC GC-CGATC-ATCC- AT-CGACCAITATCCCC GAT-CGATCAC-TCCCC	TTCGGGGGC TTCGGGGGC TTCGGGGGA TTCGGGGGA	GTGGGGATH GTGAGGGTT TATGGAGGTU GTGGAGGTC	G-GG M.phlei -GGG M.leprae -TGG M.gastri
-	1650	1660	1670	1680
1896 1896 1986 1917 1677	GGCTGCGTGGGAACTT GGCTGCGTGGGACCTT GGCTGCGTGGGACCTG GGCTGCGTGGGAACCTG GGCTGCGTGGGAACCTG	CGCTGGTAG' CGCTGGTAG' CGTTGGTAG'	TAGTCAAGCAATAGTCAAGCGATAGTCAAGCGATAGTCAAGCGATAGTCAAGCGATAGAGCGATAGCATAGCGATAGCATAGCGATAGCGATAGCGATAGCGATAGCGATAGCGATAGCGATAGCGATAGCGATAGCGATAGCATAGCGATAGCATAGATAG	ATGGG M.phlei ATGGG M.leprae
	1690	1700	1710	1720
1936 1936 2025 1957 1717	-GTGACGCAGGAAGG -GTGACGCAGGAAGG -GTGACGCAGGAAGG -GTGACGCAGGAAGG -GTGACGCAGGAAGG	DAGCCGTACO DAGCCGTACO TAGCCGTACO DAGCCGTACO	CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT	TAATA- M.phlei

Figure 1G

```
1760
                                                     1750
                    1730
                                     1740
2672 -CTGGGGCAAGCCGGTAGGGAGAGCGATAGGCAAATCCGT M.tuberculosis
2672 -CTGGGGCAAGCCGGTAGGGAGAGCGATAGGCAAATCCGT M.tuberculosis
1974 -CTGGGGCAAGCCGGTAG-AGAGCGATAGGCAAATCCGT M.avium
1974 -CTGGGGCAAGCCGGTAG-AGAGCGATAGGCAAATCCGT M.paratuberc.
2063 -CGGGGGTAAACCTGTAGGGCGACTGATAGGCAAATCCGT M.phlei
1995 -CTGGAGCAAGCCGGTAGGGAGAGCGATAGGCAAATCCGT M.leprae
1755 -CTGGGGCAAGCCAGTAGGGAGAGCGATAGGCAAATCCGT M.gastri
1698 -CTGGGGCAAGCCAGTAGGGAGAGCGATAGGCAAATCCGT M.kansasii
4149 -CGGGGTAAGCCTGTAGGGAGTCAGATAGGTAAATCCGT M.smegmatis
                                                                       2000
                                                       1990
                                      1980
                      1970
 2908 AGGGGGACCGGAATATCGTGAACACCCTTGCGGTGGGAGC M.tuberculosis
 2208 AGGGGGCCGGAATACCGTGAACACCCTTGCGGTGGGAGC M.avium
2208 AGGGGGCCCGGAATACCGTGAACACCCTTGCGGTGGGAGC M.paratuberc.
  2298 AGGGGACCCACGTACCGTGAGGCCTCTTGCGGCGGGGAGC M.phlei
  2231 AGGGGGCCGGAATATCGTGAACACCCTTGCGGTGGGAGC M.leprae
  1934 AGGGGGACCGGAATAGCGTGAACACCCTTGCGGTGGGAGC M.kansasii
4385 AGGGGGACCCACATGGCGTGTAAGCCTTTACGGCCCAAGC M.smegmatis
                                                                       2440
                                                       2430
                                       2420
                       2410
   3345 ACCTCGACGCCAGTTGGGGCGGGGGTCGTTGTTGAAATACC M.tuberculosis
   284 ACCTCGACGCCAGTTGGGGCGGAGTCGTTGTTGAAATACC M.bovis
   2645 GCACAGACGCCAGTTTGTTGTGGAGTCGTTGTTGAAATACC M.avium
           ATACAGACGCCAGTTTGTATGGAGTCGTTGTTGAAATACC M.intracellulare
   2645 GCACAGACGCCAGTTTGTGTGGAGTCGTTGTTGAAATACC M.paratuberc.
2737 GCTCGGACGCCAGTTGGGGTGGAGTCGTTGTTGAAATACC M.phlei
    2668 ACTTCGACGCTAGTTGGGGTGGAGTCGTTGTTGAAATACC M.leprae
                                                                              M.gastri
    2372 ACCTCAACGCCAGTTGGGGGTGGAGTCGTTGTTGAAATACC M.kansasii
    4822 GCTCACACGCCAGTGTGGGGGGGGGGGTCGTTGTTGAAATACC M.smegmatis
```

Figure 1H

				
	2450	2460	2470	2480
324 AC 2685 AC 433 AC 2685 AC 2777 AC 2708 AC	TCTGATCGTATTG TCTGATCGTATTG TCTGATCGTATTG TCTGATCGTATTG TCTGATCGTATTG	GACATOTAAC GACACCTAAC GACACCTAAC GGCTCTAAC GACATCTAAC	STCGAACCCI GTCGAACCCI GTCGAACCCI CTCGGACCGI	GAATC M.tuberculosis GAATC M.bovis FTATC M.avium TATC M.intracellulare TATC M.paratuberc. GGATC M.phlei FATATC M.leprae M.gastri FGAATC M.kansasii TATATC M.smegmatis
-	2490	2500	2510	2520
364 G 2724 G 472 G 2724 G 2817 R 2748 E	GGTTTAGGGACAG GGGTTCACGGACAG GGGTTCACGGACAG GGGTTCACGGACAG GGGTTCAGGGACAG	TGCC166C66 TGCCTGCC66 TGCCTGCC66 TGCCTGGGGGGGGGG	GTAGTTTAAC GTAGTTTAAC GTAGTTTAAC GTAGTTTAAC	TTGGGGC M.tuberculosis TTGGGGC M.bovis TTGGGGC M.avium TTGGGGC M.intracellulare TTGGGGC M.paratuberc. TTGGGGC M.phlei TTGGGGC M.leprae M.gastri TTGGGGC M.kansasii TTGGGGC M.smegmatis
		-		
	2930	2940	2950	2960
3163 3163 3256 3187	AGTACGAGAGGA AGTACGAGAGGA AGTACGAGAGGA AGTACGAGAGGA	CCGGGACGGA CCGGGACGGA CCGGGACGGA	CGAACCTCTG CGAACCTCTG CGAACCTCTG	GTGCACCA M.tuberculosis GTATACCA M.avium GTATACCA M.paratuberc. GGTATACCA M.phlei GGTATACCA M.leprae M.gastri AGTGCACCA M.kansasii GGTATACCA M.smegmatis

Figure 11

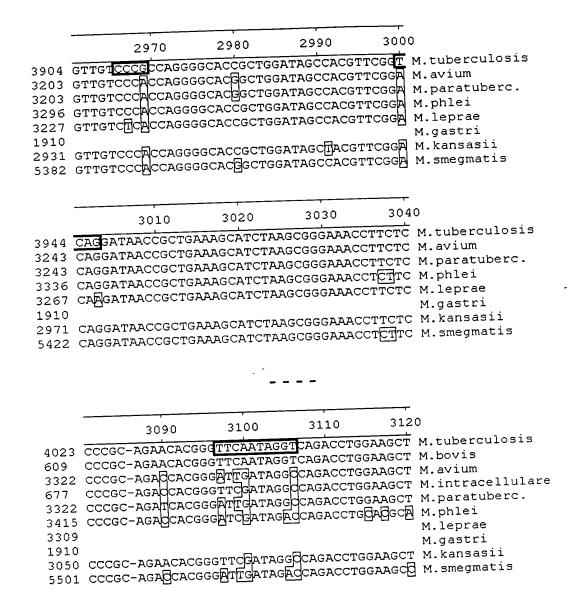
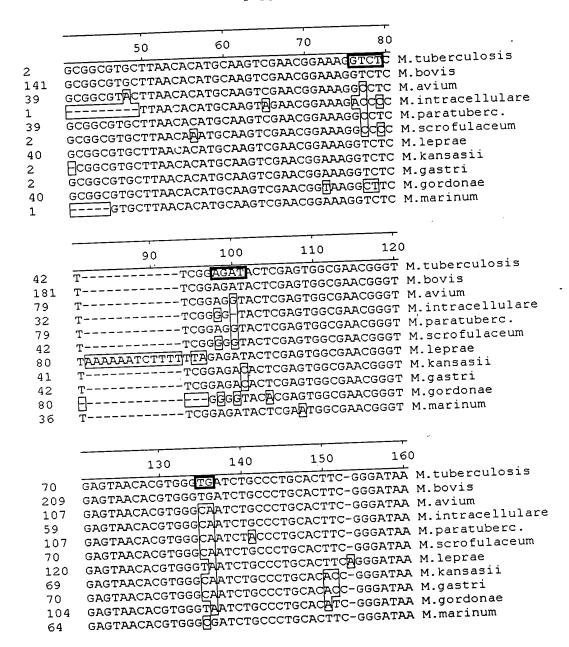
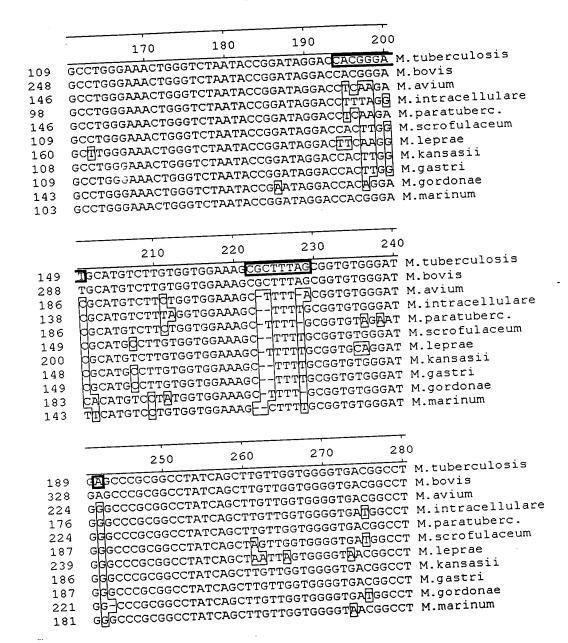


Figure 1J





450 460	470	480
AAACCTCTTTCACCATCGACGAAGCAACCTCTTTCACCATCGACGAAGCAACCTCTTTCACCATCGACGAAGCAACCTCTTTCACCATCGACGAAGCAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAAACCTCTTTCACCATCGACGAAGAAACCTCTTTCACCATCGACGAAGAAACCTCTTTCACCATCGACGAAGAAACCTCTTTCACCATCGACGAAGAAACCTCTTTCACCATCGACGAAGAAACCTCTTTCACCATCGACGAAGAAACCTCTTTCACCATCGACGAAGAAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACCATCGACGAAGAACCTCTTTCACATCGACGAAGAACCTCTTTCACAACAAAACCTCTTTCACAACAAAAAACCTCTTTCACAAAAAA	CCGGGTTITT CCGGGTTITT CCGGGTTITT CCGGGTTITT CCGGGGAATT CCGGGTTCT CCGGGTTCT	CTCGG CTCGG CTGGG CTGGG CTGGG CTCGG CTCGG CTCGG

1130 1140 1150 1160 1069 TCTCATGTTGCCAGCACGTAATGGTGGGGACTCGTGAGAG M.tuberculosis 1208 TCTCATGTTGCCAGCACGTAATGGTGGGGGACTCGTGAGAG M.bovis 1104 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.avium 1056 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.intracellulare 1098 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.paratuberc. 1064 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.scrofulaceum 1119 TCTCATGTTGCCAGCACGTAATGCCGGGGACTCGTGAGAG M.leprae 1119 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.kansasii 1066 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.gastri	1069 TCTCATGTTGCCAGCACGTAATGGTGGGGACTCGTGAGAG M.tuberculosis 1208 TCTCATGTTGCCAGCACGTAATGGTGGGGACTCGTGAGAG M.bovis 1104 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.avium 1056 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.intracellulare 1098 TCTCATGTTGCCAGCGGGTAATGCAGGGGACTCGTGAGAG M.paratuberc. 1098 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.scrofulaceum 1064 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.leprae						
TCTCATGTTGCCAGCACGTAATGGTGGGGACTCGTGAGAG M.avium 1104 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.intracellulare 1056 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.paratuberc. 1098 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.scrofulaceum 1064 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.leprae 1119 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.kansasii 1066 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.qastri	TCTCATGTTGCCAGCACGTAATGGTGGGGACTCGTGAGAG M.avium 1104 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.intracellulare 1056 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.paratuberc. 1098 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.scrofulaceum 1064 TCTCATGTTGCCAGCAGCTAATGCCGGGGACTCGTGAGAG M.leprae 1119 TCTCATGTTGCCAGCAGCTAATGCCGGGGACTCGTGAGAG M.kansasii 1066 TCTCATGTTGCCAGCAGCGGTAATGCCGGGGACTCGTGAGAG M.gastri 1067 TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG M.gordonae		1130	1140			•
		1208 1104 1056 1098 1064 1119 1066 1106	TCTCATGTTGCCAGO	ACGTAATGG ACGTAATGC GGGTAATGC GGGTAATGC ACGTAATGC ACGTAATGC GGGTAATGC	GGGGACTCGTG: GGGGACTCGTG GGGGACTCGTG GGGGACTCGTG GGGGACTCGTG GGGGACTCGTG GGGGACTCGTG GGGGACTCGTG	AGAG AGAG AGAG AGAG AGAG AGAG AGAG	M.avium M.intracellulare M.paratuberc. M.scrofulaceum M.leprae M.kansasii M.gastri M.gordonae

	•
1250 1260 1270	1280
1250 1260 1270 1189 CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTT 1328 CAATGGCCGGTACAAAGGGCTGCGATGCCGCTAAGGT 1224 CAATGGCCGGTACAAAGGGCTGCGATGCCGCAAGGT 1176 CAATGGCCGGTACAAAGGGCTGCGATGCCGCAAGGT 1218 CAATGGCCGGTACAAAGGGCTGCGATGCCGCAAGGT 1239 CAATGGCCGGTACAAAGGGCTGCGATGCCGCAAGGT 1239 CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGT 1186 CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGT 1220 CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGT 1221 CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGT 1222 CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGT 1231 CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGT	TAAG M.avium TAAG M.intracellulare TAAG M.paratuberc. TAAG M.scrofulaceum TAAG M.leprae TAAG M.kansasii TTAAG M.gastri

Figure 2C

				
	1290	1300	1310	1320
1368 C 1264 C 1216 C 1258 C 1224 C 1279 C 1226 C	CAATCCTTA-AAAGCCAATCCTTA-AAAGCCAATCCTTTTAAAAGCAATCCTTTTAAAAGCAATCCTTTTAAAAGCAATCCTTTTAAAAGCAATCCTTTTAAAAGCAATCCTTTTAAAAGCAATCCTTTTAAAAGCAAATCCTTTTAAAAGCAAATCCTTTTAAAAGCAAATCCTTTTAAAAGCCAATCCTTTTAAAAGC	CCGGTCTCAG CCGGTCTCAG CCGGTCTCAG CCGGTCTCAG CCGGTCTCAG CCGGTCTCAG CCGGTCTCAG	TTCGGATTGG TTCGGATTGG TTCGGATTGG TTCGGATCGG TTCGGATCGG TTCGGATCGG	GGTCT M.intracellulare GGTCT M.paratuberc. GGTCT M.scrofulaceum
	1330	1340	1350	1360
1407 1304 1256 1298 1264 1319 1266 1267	GCAACTCGACCCCA GCAACTCGACCCCA GCAACTCGACCCCA GCAACTCGACCCCA GCAACTCGACCCCC GCAACTCGACCCCC GCAACTCGACCCCCC GCAACTCGACCCCCC	TGAAGTCGGA TGAAGTCGGA TGAAGTCGGA TGAAGTCGGA TGAAGTCGGA TGAAGTCGGA TGAAGTCGG	AGTCGCTAGTA AGTCGCTAGTA AGTCGCTAGTA AGTCGCTAGTA AGTCGCTAGTA AGTCGCTAGTA AGTCGCTAGTA AGTCGCTAGTA	ATCGCA M.tuberculosis ATCGCA M.bovis ATCGCA M.avium ATCGCA M.intracellulare ATCGCA M.paratuberc. ATCGCA M.scrofulaceum ATCGCA M.leprae ATCGCA M.kansasii ATCGCA M.gastri ATCGCA M.gordonae ATCGCA M.marinum

Figure 2D

	50	60	70	80	
128	TTCCGAACCCGGAAC	CTAAGCCTGC	CCAGCGCCGAT	GATAC	M.tuberculosis M.bovis
39					
41 3559		~~~~~~~~~~	DC AGCCGCCGAT	CALAC	M. ICPLUC
5743	TACCGAACCCGGAA TCCCGAACCCGGAA	GCTAAGCCTG	ccagcHccga.i	rgatac	M. Smegmacis
					
	90	100	110	120	
168	TGCCCCTCCGGG	TGGAAAAG	TAGGACACCG	CCGAAC	M.tuberculosis
79	TGCCQ <u>CTCCG</u> GG- TGCCCTCCGGGG- TGCCC <u>TCA</u> CGGGG-	maannna.	maccicicacccic	CCGAAC	M.DOATS
81					
3599 5782		TGGAAAAG	TAGGACACCG	CCGAAC	M.smegmatis

Figure 3

	90	100	110	120
382	GGGAGCTGTCAACCG GGGAGCTGTCAACCG GGGAGCTGTCAACCG GGGAGCTGTCAACCG GGGAGCTGTCAACCG	AGCATTGATO AGCATTGATO AGCGTGGATO AGCGTGGATO AGCGTGGATO AGCGTGGATO AGCGTGGATO	CCGAGGATTT CCGAGGATTT CCGAGGATTT CCGAGGATTT	CCGAAT M.tuberculosi: CCGAAT M.phlei CCGAAT M.leprae

170 180 190 200 462 GAATATATAGGGTGCG-GGAGGTAACGCGGGGAAGTGAAA M.avium 462 GAATATATAGGGTGCG-GGAGGTAACGCGGGGAAGTGAAA M.paratuberc. 1133 GAATATATAGGGTGCG-GGAGGGAACGCGGGGAAGTGAAA M.tuberculosis 547 GAATATATAGGCGTTG-GGGGGAACGCGGGGAAGTGAAA M.phlei 472 GAATATATAGGGTTCG-GGAGGGAACGCGGGGAAGTGAAA M.leprae 247 GAATATATAGGGTGCG-GGAGGGAACGCGGGGAAGTGAAA M.gastri 190 GAATATATAGGGTGCG-GGAGGGAACGCGGGGAAGTGAAA M.kansasii 2628 GAATATATAGGCGTCTG-GGGGGGAACGCGGGGAAGTGAAA M.smegmatis		_				
GAATATATAGGGTGCG-GGAGGTAACGCGGGAAGTGAAA M.tuberculosis 1133 GAATATATAGGGTGCG-GGAGGGAACGCGGGGAAGTGAAA M.phlei 547 GAATATATAGGGTTG-GGGGGAACGCGGGGAAGTGAAA M.leprae 472 GAATATATAGGGTTCG-GGAGGGAACGCGGGGAAGTGAAA M.gastri 247 GAATATATAGGGTGCG-GGAGGGAACGCGGGAAGTGAAA M.gastri		170				=
2628 GAATATATAGGCGTCT-GGGGGGAACGCGGGGAAGTGAAA M. SMEGMACTS	462 1133 547 472 247	GAATATATAGGGTGCG-GAATATATAGGGTGCG-GAATATATAGGGTTGG-GAATATATAGGGTTCG-GAATATATAGGGTGCG-GAATATATAGGGTGCG-GAATATATAGGGTGCG-GAATATATAGGGTGCG-	-ggaggta -ggagga -ggagga -ggagga -ggagga	AACGCGGGGAAGTG AACGCGGGGAAGTG AACGCGGGGAAGTG AACGCGGGGGAAGTG	AAA AAA AAA AAA	M.tuberculosis M.phlei M.leprae M.gastri M kansasii

	250	260	270	280	
	-GTCAGTAGTGGC	TACCCATIC-CGG	DACA-GGCTA	AAACCG	M.avium
541·	-GTCAGTAGTGGCC	JAGCGAA <u>C CCC</u>	AACA-GGCT	AAACCG	M.paratuberc.
541	-GTCAGTAGTGGC		TARCA GGCTI	DDACCG	M.tuberculosis
1212	-GCAAGTAGTGGC	GAGCGAACGCG	AACA-GGCT	NDDCCG	M.tuberculosis M.phlei
626	-GEAGTAGTGGC -GTGAGTAGTGGC	GAGCGAALAGG	AGGAIIGGCI	חחחררה	M leprae
551	-GTGAGTAGTGGC -GCAAGTAGTGGC	GAGCGAACGIG	SAAIIAIIGGCI.		M dastri
326	-GCAAGTAGTGGC -GTCAGTAGTGGC	GAGCGAACGCG	GAACAIIGGCI	AAACCG	M kansasii
260	-GTCAGTAGTGGC -GTAAGTAGTGGC	GAGCGAACGCG	GAACANGGCT	дддССС	M. Addisabil
209	-gtaagtagtggc Ggtgagtagtggc	CAGCGAACACG	GAGGATGGCT	AAAC G	M.smegmacis
2706	De Leve Lye 1996	0.1000.00			

Figure 4A

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310
                                                     320
                290
     CATG-CATGGACAACCGGGTAGGGGTTGTGTGTGCGGGGT M.avium
      CATG-CATGGACAACCGGGTAGGGGTTGTGTGTGCGGGGT M.paratuberc.
1250 CAGG-CATGGGTAACCGGGTAGGGGTTGTGTGTGCGGGGT M.tuberculosis
      сете-сатегейдассеетечестветечестве м.phlei
664
      CACA-CATGECTAACTAGGTAGGGGTTGTGTGTGCGGEGT M.leprae
590
      CAGE-CATGGGTGACCGGGTAGGGGTTGTGTGTGCGGGGT M.gastri
365
      CAGG-CATGGGTACCGGGTAGGGGTTGTGTGTGCGGGGT M. Kansasii
308
2745 TATGACATGTGATACCGGGTAGGGGTTGTGTGTGCGGGGT M.smegmatis
                                                       360
                                          350
                              340
                 330
      TGTGGGATTGATATGTCTCAGGTCTACCTGGCTGAGG-GG M.avium
TGTGGGATTGTTCTCAGCTCTACCTGGCTGAGG-GG M.paratuberc.

1289 TGTGGGAG-GATATGTCTCAGCGCTACCTGGCTGAGG-GG M.tuberculosis

TGTGGGGCCTGTGTGTCCTCATCGTCCGCCGGCGATGGCAG M.phlei

TGTGGGGATTGTATGTCTCAACTCTACCTGGTTGAGG-GG M.leprae
       TGTGGGATGGATACGTCTCAGCTCTACCCGGCTGAGG-GG M.gastri
TGTGGGATCGATACGTCTCAGCTCTACCCGGCTGAGG-GG M.kansasii
 404
 2785 TGTGGGACCTATGTTTC-CGCTCTACCTGGCTG-GAGGG M.smegmatis
                                                       400
                                           390
                              380
                  370
       TAGTCAGAAAGTGTCGTGGTTAGCGGAAGTGGCCTGGGAC M.avium
 656 TAGTCAGAAAGTGTCGTGGTTAGCGGAAGTGGCCTGGGAC M.paratuberc.
 1327 GAGTCAGAAAGTGTCGTGGTTAGCGGAAGTGGCCTGGGAT M.tuberculosis
       TAGTEATTAAAGEAGTGTGGTTAGETGAAGTGGCCTGGGAT M.phlei
        TAGTCAGAAAGTGCCGTGGTTAGCGGAAATGGCCTGGGAT M.leprae
        CAGTCAGAAAGTGTCGTGGTTAACGGAAGTGGCCTGGGAT M.gastri
CAGTCAGAAAGTGTCGTGGTTAACGGAAGTGGCCTGGGAT M.kansasii
  443
  2823 CAGTGAGAAAATGTTTGTGGTTAGCGGAAATGGCTTTGGGAT M.smegmatis
```

Figure 4B

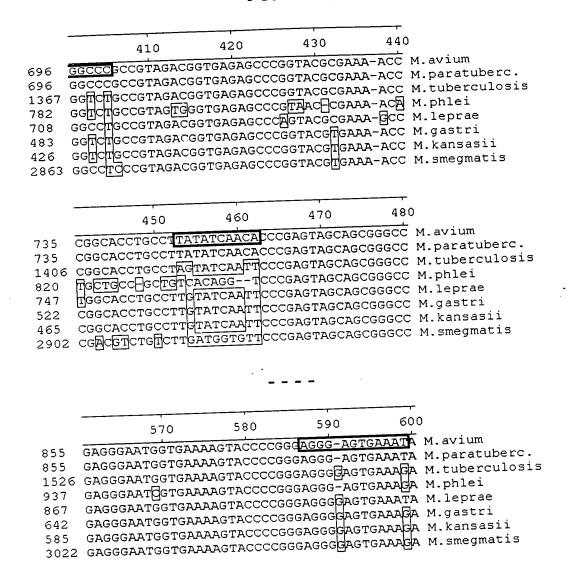


Figure 4C

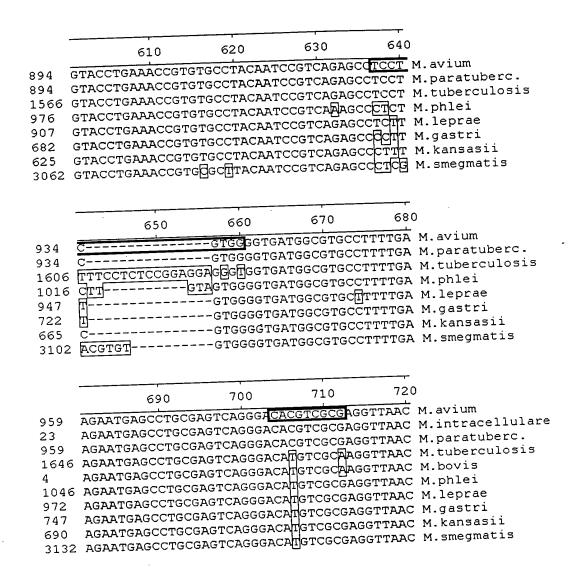


Figure 4D

				
	770	780	790	800
			GTGTAGTGG	CGTGT M.avium
	CATCCCCTTTGGG- CATCCCCTTTGGG-		CTCTAGTGG	CGTGT M.intracellulare
			~m~m~cm^c()	ramam M naratuberc.
		T CCCCCCCC	ನ್ನಡ್ಡಾಗ್ಡ್ <u>ಸ್</u> ವರ್ಗ	CGTGT M.tuberculosis
1126 0	GACOCACACOTORT GRATCCAACOTORT	= = = = (2(2(2))')'	ALTERNATION OF	IO IO I III F
1052 C	GHATCACGTGTGAGK	CG/I/		
827 C	GHATCACGCGTAAGI	CGT	-GTGTAGTGG	CGTGT M.gastri
770 C	GHATCGCGCGCGAG	CGT	-GTGTAGTGG	CGTGT M.kansasii
3212 C	GTATCCACACAAGA	GTGTGTG	-GTGTAGTGG	GTGT M.smegmatis
-		1000	1070	1080
	1050	1060		Emagga M avium
1307	CAGCCAAACTCCGA	ATGCCG-TGG	TG-TAAAAGC	GTGGCA M.avium
1307	CAGCCAAACTCCGA	ATGCCG-TGG	TG-TAAAAGC	GTGGCA M.paratuberc.
2005	CAGCCAAACTCCGA	ATGCCG-TGG	TG-TA-AAGC	GTGGCA M.tuberculosis
1401	CAGCCAAACTCCGA	ATGCCGATAA		GTGGCA M.leprae
1323	CAGCCAAACTCCGA	ATGCCG-TGG		COTCCCA M. dastri
1098	CAGCCAAACTCCGA	ATGCCG-1GC	TO THE CO	ramagan M.kansasii
1041	CAGCCAAACTCCGA	ATGCCG-190	GCCAAGAG	GGGGA M.smegmatis
3486	CAGCCAAACTCCGA	MIGCCGGIP	<u> </u>	
		_		
				1000
	1170	1180	1190	1200
	TOMOGRAPANCENT	GTGTAGTCGC	AGA-GACAAC	CAGGAGG M.avium
1425	AGTGGAAAAGGAT	GTGTAGTCGC	AGA-GACAAC	CAGGAGG M.paratuberc.
1423	AGTGGGAAAGGAT	GTGCAGTCGC	:AAA-GACAAC	CCAGGAGG M.tuberculosis
1510	AGTGGAAAAGGAT	GTGCAGTCGC	:EgaAgacaa(CCAGGAGG M.phlei CCAGGAGG M.leprae
1 4 4 1	AGTGGAAAAGGAT	GTGCAGTCGC	AAA-GACAA	CCAGGAGG M.leprae
1215	AGTGGGAAAGGAT	GTGCAGTCGC	CAGA-GACAA	CCAGGAGG M.gastri
1158	AGTGGGAAAGGAT	GTGCAGTCG	CAGA-GACAA	CCAGGAGG M.kansasii
3606	S AGTGGĀAAAGGAT	rgtg p agtcg	CAGAMGAMAA	CCAGGAGG M.smegmatis

			1070	1280	
	1250	1260	1270		
504 CTCA 201 CTCA 598 CTCA 520 CTCA 294 CTCA	CTGGTCAAGTG CTGGTCAAGTG CTGGTCAAGTG CTGGTCAAGTG CTGGTCAAGTG ACTGGTCAAGTG ACTGGTCAAGTG	ATTATGCGCC ATTGTGCGC[] ATTGTGCGCC ATTGTGCGCC	GATAATGTAG GATAATGTAG GATAATGTAG GATAATGTAG	CGGGG M CGGGG M CGGGG M	.tuberculosis .phlei .leprae .gastri
	1290	1300	1310	1320	
544 CTC	AAGCACACCGC	CGAAGCCGCG	CACATTCAT	CTT-TA N	M.avium M.paratuberc.
		マベカカ こここににい	-CACACICAI	OII IN .	M.paratuberc. M.tuberculosis
2241 CTC	AAGCACACCGC AAGCACACCGC AAGCACACCGC	CGAAGCCGCG	SCAF-ATCAG		M.phlei
1638 CTC	AAGCACACCGC AAGCACACCGC	CGAAGCCGCG	GCACATTCAC		M.leprae
1560 CTC	AAGCACACCGC AAGCACACCGC	CGAAGCCGCG	ACAFAC		M.gastri
		CCDDGCCGCG	MCAL PA		M.kansasii
3726 TTC	;AAGCACACCGC ;AAGCACACCGC	CGAAGCCGCG	GAAGCAE	CGTUTG	M.smegmatis
					_
	1330	1340	1350	136	
1502 000	TGGA TGTGGGT	AGGGGAGCGT	CCCCCATTC	AGCGAAG	M.avium
1583 <u>CGC</u> 1583 CGC	TGGATGTGGGT	AGGGGAGCGT	CCCCCATTC	AGCGAAG	M.paratuberc. M.tuberculosi
1600 GG		raggggagcg' raggggagcg'			
	GTTGGG	raggggagce [.] 	rcccrcaTTC	AGCGAAG	M.kansasii
1310 AG	GTTGGG'	TAGGGGAGCG		GGTGAAG	M.smegmatis
3764 TT	TGGG'	TAGGGGAGCG	TOOTTO INTER	E-E	-

Figure 4F

						
-	137		380	1390	1400	
1623 (2319 (1716 (1640 (1402 (CACCEGETG CCCCCCEGETA CCCCCCCEGETA CCCCCCCCC	ANCGGTGG ACCGGTGG ANCGGTGG ACCGGTGG ACCGGTGG	TGGAGGGT TGGAGGGT TGGAGGGT TGGAGGGT	ggggagtga ggggagtga ggggagtga ggggagtga ggggagtga	GAAT 1 GAAT 1 GAAT 1 GAAT 1	M.tuberculosis M.phlei M.leprae
	15	30	1540	1550	156	
1781 2479 1875 1800 1562	CGATGGACA CGATGGACA CGATGGACA	ACGGGTTG ACGGGTTG ACGGGTTG ACGGGTTG ACGGGTTG	ATATTCCCG ATATTCCCG ATATTCCCG ATATTCCCG	TACCCGTGT TACCCGTGT TACCCGTGT TACCCGTGT	GTGGG ATGAG GTGIG GTGGG	M.tuberculosis M.phlei M.leprae
	1	570	1580	1590	160	
1821 2519 1915	CGDCCGTG7 CGTCCCTG7 CGCCCGTG7 CGCCCGTG7	ATGAATCA- AGGAATCA- ATGAATCA- ATGAATCA- ATGAATCA-	-GCGGTACT -GCGGTACT -GCGGTACT	AACCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AAACCE AAACCE AAACCE AAACCE	M.tuberculosis M.phlei M.leprae

Figure 4G

				
	1.610	1620	1630	1640
	1610	1020		
1860	GAT-CGACCAT-TCC	CCTTCGGGGG	C-GTGGCGATT	-CFG M.avium
1860	GAT-CGACCAT-TCC	CCTTCGGGGG	C-GTGGCGATT	C-CGG M.paratuberc.
2558	GAT-CGATICAD-TCC	CCTTCGGGGG	-TGTGGAGITE	Ingg M. tuberculosis
1955	GGG-CGATCF-ATCC	F-TTCGGGGE	GTGACGGTT	- GG M.tuberculosis G-GG M.phlei
1979	GAT-CGACCATATCC	CCTTCGGGGG	CTATGGAGGTI	r-CGG M.leprae
16/1	GAT-CGATICATCC GAT-CGATICAC-TCC	CCTTCGGGGG	A-GTGGAGGTK	d-ПGG M.gastri
150/	CAT-CGAMCAC-TCC	CCTTCGGGGG	c-gregaggtk	-ngg M.kansasii
1005	ECCETCA CCECACCT	rrcggggF	-TGTGGCGNT	GGTGG M.smegmatis
4033	ACCO TOROGESTS			
				1.690
	1650	1660	1670	1680
1000	GGCTGCGTGGGACCT	TTCGCTGGTAG	TAGTCAAGCA	ATGGG M.avium
1917	GGCTGCGTGGGAAC	ruccentente.	TAGTORISCO	ATGGG M.gastri ATGGG M.kansasii ATGGG M.smegmatis
1677	GGCTGCGTGGAGCC	TTCGCTGGTAC	TAGTCAAGCG	ATGGG M.kansasii
1620	GGCTGCGTGGAGCC		TAGICARGO	ATGGG M.smegmatis
4071	GGCTGCATGGGACC'	TTCGITTGGTAG	TAGICAAGCE	Aldo III January
		1700	1710	1720
	1690	1700	1710	1720
1936		aca acacama co	TAGTCAGTGGT	TAATA- M.avium
	-GTGACGCAGGAAG	GCAGCCGTAC	CAGTCAGTGGT	TAATA- M.avium
1936	-GTGACGCAGGAAG -GTGACGCAGGAAG	GCAGCCGTAC	CAGTCAGTGGT CAGTCAGTGGT	TAATA- M.avium TAATA- M.paratuberc. TAABA- M.tuberculosis
1936 2634	-GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG	GCAGCCGTACO GCAGCCGTACO GTAGCCGTACO	CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT	M.avium TAATA- M.avium TAATA- M.paratuberc. TAADA- M.tuberculosis TAATA- M.phlei
1936 2634 2025	-GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG	GCAGCCGTACO GCAGCCGTACO GTAGCCGTACO	CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT	M.avium TAATA- M.paratuberc. TAAGA- M.tuberculosis TAATA- M.phlei TAATA- M.leprae
1936 2634 2025 1957	-GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG	GCAGCCGTACO GCAGCCGTACO GTAGCCGTACO GTAGCCGTACO	CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT	M.avium TAATA- M.paratuberc. TAAGA- M.tuberculosis TAATA- M.phlei TAATA- M.leprae TAATA- M.gastri
1936 2634 2025 1955 171	-GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG	GCAGCCGTACO	CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT	M.avium TAATA- M.paratuberc. TAACA- M.tuberculosis TAATA- M.phlei TAATA- M.leprae TAATA- M.gastri TAATA- M.kansasii
1936 2634 2025 1955 171	-GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG	GCAGCCGTACO	CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT	M.avium TAATA- M.paratuberc. TAACA- M.tuberculosis TAATA- M.phlei TAATA- M.leprae TAATA- M.gastri TAATA- M.kansasii
1936 2634 2025 1955 171	-GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG	GCAGCCGTACO	CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT	M.avium TAATA- M.paratuberc. TAAGA- M.tuberculosis TAATA- M.phlei TAATA- M.leprae TAATA- M.gastri
1936 2634 2025 1955 171	-GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG	GCAGCCGTACO	CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT	M.avium M.paratuberc. M.paratuberc. M.paratuberc. M.tuberculosis M.phlei MATA- M.leprae MATA- M.gastri MATA- M.kansasii MATA- M.smegmatis
1936 2634 2025 1957 1717 1660 4117	-GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG	GCAGCCGTACO GCAGCCGTACO GTAGCCGTACO GCTAGCCGTACO GCAGCCGTACO GCAGCCGTACO GCAGCCGTACO GCAGCCGTACO GCAGCCGTACO GCAGCCGTACO GCAGCCGTACO	CAGTCAGTGGT	M.avium M.paratuberc. M.sastri M.sassii M.smegmatis M.smegmatis
1936 2634 2025 1951 1711 1660 4111	-GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG -GTGACGCAGGAAG	GCAGCCGTACO GCAGCCGTACO GTAGCCGTACO GCAGCCGTACO GCAGCCGTACO GCAGCCGTACO GCAGCCGTACO GCAGCCGTACO GCAGCCGTACO GCAGCCGTACO GCAGCCGTACO GCAGCCGTACO GCAGCCGTAC	CAGTCAGTGGT CAGTCA	M. avium M. paratuberc. M. p
1936 2634 2025 1951 1711 1660 4111	-GTGACGCAGGAAG	GCAGCCGTACO GCAGCCGTACO GTAGCCGTACO GCAGCCGTACO	CAGTCAGTGGT CAGTTAGGCAA	M. avium M. paratuberc.
1936 2634 2025 1957 1717 1660 4117	-GTGACGCAGGAAG -CTGGGGCAAGCC	GCAGCCGTACO GCAGCCGTACO GTAGCCGTACO GCAGCCGTACO ACO	CAGTCAGTGGT CAGTAGGCAA	M. avium M. AATA- M. paratuberc. M. AATA- M. tuberculosis M. AATA- M. Phlei M. AATA- M. leprae M. AATA- M. kansasii M. AATA- M. Smegmatis ATCCGT M. avium ATCCGT M. paratuberc. ATCCGT M. tuberculosis
1936 2634 2025 1957 1717 1660 4117 197 197 267	-GTGACGCAGGAAG -CTGGGGCAAGCC -CTGGGGCAAGCC	GCAGCCGTACO GCAGCCGTACO GTAGCCGTACO GCAGCCGTACO ACACO GCAGCCGTACO GCACCCGTACO GCACCCCCCCCCCCCCCCCCC GCACCCCCCCCCCC	CAGTCAGTGGT CAGTCAGTAGGCAA	TAATA- M.avium TAATA- M.paratuberc. TAADA- M.tuberculosis TAATA- M.phlei TAATA- M.leprae TAATA- M.gastri TAATA- M.kansasii TAATA- M.smegmatis 1760 ATCCGT M.avium ATCCGT M.paratuberc. ATCCGT M.tuberculosis
1936 2634 2025 1957 1660 4111 197 197 267 206	-GTGACGCAGGAAG -CTGGGGCAAGCC -CTGGGGCAAGCC -CTGGGGCAAGCC	GCAGCCGTACO GCAGCCGTACO GTAGCCGTACO GCAGCCGTACO GCACCCGTACO GCACCCCCCCCCCCCCCC GCACCCCCCCCCCCCCC	CAGTCAGTGGT CAGTCAGTAGGCAA	TAATA- M.avium TAATA- M.paratuberc. TAABA- M.tuberculosis TAATA- M.phlei TAATA- M.leprae TAATA- M.gastri TAATA- M.kansasii TAATA- M.smegmatis 1760 ATCCGT M.avium ATCCGT M.paratuberc. ATCCGT M.tuberculosis ATCCGT M.phlei
1936 2634 2025 1957 1660 4111 197 197 267 206	-GTGACGCAGGAAG -CTGGGGCAAGCC -CTGGGGCAAGCC -CTGGGGCAAGCC	GCAGCCGTACO GCAGCCGTACO GTAGCCGTACO GCAGCCGTACO GCACCCGTACO GCACCCCCCCCCCCCCCC GCACCCCCCCCCCCCCC	CAGTCAGTGGT CAGTCAGTAGGCAA	TAATA- M.avium TAATA- M.paratuberc. TAABA- M.tuberculosis TAATA- M.phlei TAATA- M.leprae TAATA- M.gastri TAATA- M.kansasii TAATA- M.smegmatis 1760 ATCCGT M.avium ATCCGT M.paratuberc. ATCCGT M.tuberculosis ATCCGT M.phlei
1936 2634 2025 1957 1660 4113 197 197 267 206 199	-GTGACGCAGGAAG -CTGGGGCAAGCC -CTGGGGCAAGCC -CTGGGGCAAGCC -CTGGGGCAAGCC	GCAGCCGTACO GCAGCCGTACO GTAGCCGTACO GTAGCCGTACO GCAGCCGTACO GCACCCGTACO GCAGCCGTACO GCACCCGTACO GCACCCCCCCCCCCCC GCACCCCCCCCCCCCCCCC	CAGTCAGTGGT CAGTTAGGCAA CAGTTAGGCAA CAGTTAGGCAA	TAATA- M.avium TAATA- M.paratuberc. TAABA- M.tuberculosis TAATA- M.phlei TAATA- M.leprae TAATA- M.gastri TAATA- M.kansasii TAATA- M.smegmatis 1760 ATCCGT M.avium ATCCGT M.paratuberc. ATCCGT M.tuberculosis ATCCGT M.phlei ATCCGT M.leprae
1936 2634 2025 1957 1660 4113 197 267 206 199	-GTGACGCAGGAAG -CTGGGGCAAGCC -CTGGGGCAAGCC -CTGGGGCAAGCC -CTGGGGCAAGCC -CTGGGGCAAGCC -CTGGGGCAAGCC -CTGGGGCAAGCC -CTGGGGCAAGCC	GCAGCCGTACO GCAGCCGTACO GTAGCCGTACO GTAGCCGTACO GCAGCCGTACO GCACCCGTACO GCACCCCCCCCCCCCC GCACCCCCCCCCCCCCCCC	CAGTCAGTGGT CAGTCAGTAGGCAA CAGTAGGCAA CAGTAGGCAA CAGTAGGCAA CAGTAGGCAA CAGTAGGCAA	TAATA- M.avium TAATA- M.paratuberc. TAADA- M.tuberculosis TAATA- M.phlei TAATA- M.leprae TAATA- M.gastri TAATA- M.kansasii TAATA- M.smegmatis 1760 ATCCGT M.avium ATCCGT M.paratuberc. ATCCGT M.tuberculosis

Figure 4H

	1810	1820	1830	1840	
	CG-AATTCGGTG	ATCCTCTGCTGC	CAAGAAAAGC	CTCTA- M	.avium
2051	CG-AATTCGGTG CG-AATTCGGTG	ATCCTCTGCTGC	CAAGAAAAGC	CCTCTA- M	.paratuberc.
2.051	CG-AATTCGGTG	ALCCICIOCO AMECUTOTO	CAAGAAAAG	CCTCTA- M	tuberculosis
2751	CG-AATTCGGTG	ATCCTCTGCTG	de Enganage	CCTCTA- M	.phlei
2141	CG-AATTCGGTC CG-AATTCGGTC CG-AATTCGGT	ATCCTATGCTG		CTCTA- M	leprae
2074	CG-AATTCGGT	AMCCACACACACA	CAAGAAAA	CCTCTA- N	. dastri
1834	CG-AATTCGGT(FATCCTCTGCTG	COAAGAAAAG	CCTCTA .	K kansasii
1777	CG-AATTCGGT(CG-AATTCGGT(SATCCTCTGCTG	CCAAGAAAAG	CCTCTA- N	M smeamatis
4228	CG-AATTCGGT(CG-AATTCGGT(SATCCTATGCTG	CCGAGAAAAG	CCTCTA- F	1. Smegmao25
	1850	1860	1870	1880 	
2000	GCGAGCACATAG	CACGGCCCGTAC	CCCAAACCAA	CACAGGT N	1.avium
2089	CCCACACATA	CACHGCCCGTAC	CCCAAACCAA	CACAGGT 1	1.paratuberc. 1.tuberculosis
2089	GCGAGCACATA	CACGGCCCGTAC	CCCAAACCGA	CACAGGT N	1.parutubero 1.tuberculosis 1.phlei
2789	GCGAGCACACA GCAAGCGCATA	CACCCCCGTAC	CCCAAACCAA	CACAGGT 1	4.phlei
2179	GCAAGCGCATA GCGAGCA∏AGA	TCCCCCCCTAC	CCCAAACCGA	CACAGGT 1	M.leprae
2112	GCGAGCATACA GCGAGCACACA	TGCGGCCCGTAC	CCAAACCGA	CACAGG 1	M.gastri
1872	GCGAGCACAGA		CCCAAACCGA	CACAGGT !	M.kansasii
1815	GCGAGCACACA GCGAGCACACA	CACGGCCCGTAC	CCCAAACCAA	CACAGGT	M.smegmatis
4266	gcgagcacada gcgaggacata	CACGGCCCGTAC	,CCAAACCA	.07.07.10 =	_
	197	0 1980	1990	200	
			TACCCTTGCG(TGGGAGC	M.avium
220	B AGGGGGCCCGC	BATACCGTGAA	CACCCTTGCC	GTGGGAGC	M.paratuberc. M.tuberculosis
220	8 AGGGGGCCCG	GAATACCGIGAA	aaammacca	CTCCGAGC	M.tuberculosis
290	8 AGGGGGACCG 8 AGGGGGACCC	GAATATCGTGAA	CACCCTTGCG	cAccAncc	M phlei
229	8 AGGGGGACCC	ACGTACCGTGAG	GGCIICTTGCG	ancearec	M lenrae
223	8 AGGGGGACC <u>C</u> 1 AGGGGGGCCG	GAATATCGTGAA	CACCCTTGCG	GIGGGAGO	M.gastri
191	n				M kansasii
193	0 4 agggggaccg 5 agggggaccc	GAATACCGTGAA	<u>CA</u> CCCTTGCG	GTGGGAGC	M. cmcqmatis
438	5 AGGGGGACCE	ACATGGCGTGTA	AGCCTTTACG	GCCCAAGC	M.Smegmaers
430	J				
				20	10
	20	10 2020	2030		
224	20 18 GGGATTCGG	CGCAGAAACCA	TGGGT AGCG	ACT-GTTTP	M.avium
22	19 GGGATTCGGC	CGCAGAAACCA	gTGGGTAGCG	ACT-GTTT	M.paratuberc. M.tuberculosis
22	10 GGGATHGGG	TCGCAGAAACCA	gtgaggagcg:	ACT-GTTT <i>F</i>	M.tuberculosis A.M.phlei
29	so ceceendee	TGGCAGAAACCA	gtg a g aacg:	ACT-GTTT	A M.pniei
23	48 GGGATÖCGG 38 GGGGGTÖGG 71 GGGATÖCGG	TCCCAGAGACCA	gtglalglalagcg.	ACT-GTTT	A M. Leprae
22	11 GGGWIMCGG	Togovovovo.			M.gastri
19	10 74 GGGATTCGG	HCCCNGNAACCA	GTGAGAAGCG	ACTRGTTT	A M.kansasii
19	74 GGGATTCGG		GTGAGAAGCG	ACT-GTTT	A M.smegmatis
44	25 GMGAGTGGG	TRICHUAAACCA	O TOBODA		

Figure 4I

				
-	2130	2140	2150	2160
2267 6	CCGTTAACCCGT	-AAGGGTGAAGC	GGAGAATTTA	AGCCC M.avium
2301	CGTTARCCGCTT	-AAGGGTGAAGC	GGAGAATTTA	AGCCC M.paratuberc.
2390		-AAGGGTGAAGC	GGAGAATTTA	
2390	Cligatawooood	•		M.gastri
1910	cccmmaacccGD-	-AAGGGTGAAGC	GGAGAATTTA	AGCCC M.kansasii AGCCC M.smegmatis
2094	CCGTTAACCCCCCT	TGGGGGTGAAGC	GGAGAATTTA	AGCCC M.smegmatis
4544	CCG1174.000[<u>0-1-</u>			
	2250	2260	2270	2280
	1		CARTA CACTO	CCGAA M.avium
2485	GTAACGACTTCC	CAACTGTCTCAA	CCNUNCACTO	GGCGAA M.avium GGCGAA M.paratuberc. GGCGAA M.tuberculosis
2485	GTAACGACTTCC	CAACTGTCTCAA	CCAIAGACIC	GGCGAA M.tuberculosis
2577				
2508	GTAACGACTTCI	CAACTGTCTCAA	CCATAGACTO	GGCGAA M.leprae M.gastri
1910			CCDUBGACTC	cccan M.kansasii
2212	GTAACGACTTCT	CAACTGTCTCAA	OTDABATADO.	GGCGAA M.kansasii GGCGAA M.smegmatis
4663	GTAACGACTTCT	CAACTGTCTCAA	CDAINGACIO	. ,
		-		
	2370	2380	2390	2400
			AGGTGGGAGAG	TTTGAA M.avium
2605	GTTCGGTACGG	TTTGIGIAGGAI TTTGIGIAGGAI	AGGTGGGAGA	CTTTGAA M.paratuberc.
2605				
	GTTCGGTACGG	TTTGTGTAGGAT.	AGGTGGGAGA'	CTGTGAA M.phlei
2697	7 GOTCGATACGG	TTTGIGIAGGAI mmmcmcmAGGAT	AGGTGGGAGA AGGTGGGAGA	
2628	3 GTTCGGTGCGG	T.L.L.G.I.G.I.W.G.W.I.	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	M.gastri
1910)	тттстстъссът	'AGGTGGGAGA	CTGTGAA M.kansasii CTGTGAA M.smegmatis
	2 GTTCGGTACGG	TTTGTGTAGGAT	AGGTGGGAGA	CTGTGAA M.smegmatis
4783	2 GOTCGATACGG	TITIGIGIAGGAI	7001000	<u> </u>

Figure 4J

				
	2410			2440
393 AT 2645 GC 3345 AC 284 AC 2737 GC 2668 AC	CACAGACGCCAGTT CTCGACGCCAGTT CTCGACGCCAGTT CTCGACGCCAGTT CTCGACGCCAGTT	TGTMTGGAGTCG TGTGTGGAGTCG GGGGCGGAGTCG CGGGTGGAGTCG GGGGTGGAGTCG	TTGTTGAAATA TTGTTGAAATA TTGTTGAAATA TTGTTGAAATA TTGTTGAAATA	ACC M.paratuberc. ACC M.tuberculosis ACC M.bovis ACC M.phlei
-	2450	2460	2470	2480
433 F 2685 F 3385 F 324 F 2777 F 2708 F	ACTCTGATCGTATT ACTCTGATCGTATT ACTCTGATCGTATT ACTCTGATCGTATT ACTCTGATTGTATT	GGACACCTAACG GGGCATCTAACG GGGCATCTAACC GGGCETCTAACC	TCGAACCCT—T TCGAACCCTGA TCGAACCCTGA TCGGACCGTGG TCGAACCGTA	ATC M.paratuberc. ATC M.tuberculosis ATC M.bovis
	2690	2700	2710	2720
2924 3625 3017 2948 1910	GGTGTCACTCAAC GGTGTCGCTCAAC GGTGTCGCTCAAC	CGGATAAAAGGTA CGGATAAAAGGTA CGGATAAAAGGTA	ACCCCGGGGAT ACCCCGGGGAT ACCCCGGGGAT	TAACAG M.avium TAACAG M.paratuberc. TAACAG M.tuberculosis TAACAG M.phlei TAACAG M.leprae M.gastri TAACAG M.kansasii TAACAG M.smegmatis
	2730	2740	2750	2760
2964 3665 3057 2988 1910	GCTGATCTTCCC GCTGATCTTCCCC GCTGATCTTCCCCCCCCCC	CAAGAGTCCATA CCAAGAGTCCATA CCAAGAGTCCATA CCAAGAGTCCATA	ATCGACGGGAT ATCGACGGGAT ATCGACGGGAT	GGTTTG M.avium GGTTTG M.paratuberc. GGTTTG M.tuberculosis GGGTTTG M.phlei GGGTTTG M.leprae M.gastri GGTTTG M.kansasii GGTTTG M.smegmatis

Figure 4K

```
2800
                                      2790
               2770
                           2780
3004 GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA M.avium
3004 GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA M.paratuberc.
3705 GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA M.tuberculosis
3097 GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA M.phlei
3028 GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGAAGCA M.leprae
                                                       M.gastri
2732 GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA M.kansasii
5182 GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA M.smegmatis
                                       2830
                                                   2840
                           2820
               2810
3044 GGTCCCAAAGGTTGGGCTGTTCGCCC-ATTAAAGCGGCAC M.avium
3044 GGTCCCAAGGTTGGGCTGTTCGCCC-ATTAAAGCGGCAC M.paratuberc.
3745 GGTCCCAAGGGTTGGGCTGTTCGCCC-ATTAAAGCGGCAC M.tuberculosis
3137 GGTCCCAAGGGTTGGGCTGTTCGCCC-ATTAAAGCGGCAC M.phlei
3068 GGTCCCAAGGGTTGGGCTGTTCGCCC-ATTAAAGCGGCAC M.leprae
1910
2772 GGTCCCAAGGGTTGGGCTGTTCGCCC-ATTAAAGCGGCAC M.kansasii
5222 GGTCCCAAGGGTTGGGCTGTTCGCCCGATTAAAGCGGCAC M.smegmatis
                                                   3080
                                       3070
                           3060
                3050
 3283 CAAGATCAGGTTT-CTCACCCTTTTTAGAGGGATAAGGCCC M.avium
 638 CAAGATCAGGTTT-CTCACCCTTTTAGAGGGGATAAGGCCC M.intracellulare
 3283 CAAGATCAGGTTT-CTCACCCTTTTAGAGGGGATAAGGCCC M.paratuberc.
 3984 CAAGATCAGGTTT-CTCACCCACTTGGTGGGATAAGGCCC M.tuberculosis
570 CAAGATCAGGTTT-CTCACCCACTTGGTGGGATAAGGCCC M.bovis
3376 CAAGACCAGGCTT-CTCACCCTCTAGGAGGGGATAAGGCCC M.phlei
                                                       M.leprae
 3307 CAA
                                                       M.gastri
 1910
 3011 CAAGATCAGGOTT-CTCACCCACTTGGTGGGGATAAGGCCC M.kansasii
5462 CAAGAGCAGGOTT-CTCACCCTGTAGGAGGGGATAAGGCCC M.smegmatis
                                                    3120
                                        3110
                            3100
                3090
  3322 CCCGC-AGACCACGGGATTGATAGGCCAGACCTGGAAGCT M.avium
  677 CCCGC-AGACCACGGGTTCGATAGGCCAGACCTGGAAGCT M.intracellulare
  3322 CCCGC-AGATCACGGGATTGATAGGCCAGACCTGGAAGCT M.paratuberc.
  4023 CCCGC-AGAACACGGGTTCAATAGGTCAGACCTGGAAGCT M.tuberculosis
609 CCCGC-AGAACACGGGTTCAATAGGTCAGACCTGGAAGCT M.bovis
3415 CCCGC-AGACCACGGGATCGATAGACCAGACCTGTAGGCA M.phlei
  3309
                                                        M.gastri
  1910
  3050 CCCGC-AGAACACGGGTTGGATAGGCCAGACCTGGAAGCT M.kansasii
  5501 CCCGC-AGACCACGGGATTGATAGACCAGACCTGGAAGCO M.smegmatis
```

Figure 4L

	130	140	150	160	
107	GAGTAACACGTGGGC	ATCTGCCCT	GCACTTC-GG	GATAA M.avium	
59			CCNC'''' - 1-1-	THAT AA MI DALACADOLO	
107					
70	GAGTAACACGTGGGG	AATCTGCCCT	CCACTIC GC	GGATAA M.tuberculosis	
70	GAGTAACACGTGGG	rgatctgccct	GCACTIC GC	COMPAN M howis	
209	GAGTAACACGTGGG GAGTAACACGTGGG	rgatctgccct	GCACTTC-GG	GAIAA M.DOVID	
120					
69		っちゃ かんかんさんしん	1-1 4 4 4 4 7 7 7	JURIAR II. Kuiluu – –	
70		~~ ~ @ @ @ @ @ @ @ @	にっしゅ しゅしん ニーしゃし	GRIAR M. GUDUU	
104	CACHARACACTECCO	- Parcinceci	GCACTTC-G	GGATAA M.marinum	
64	GAGTAACACG1600	OD, 1. 0. 1. 0. 1. 1.	_		
			_		
		-			
				_	
	450	460	470	480	
		- maga can ac	בתררפים חדיו	TTCTCGG M.avium	
424	AAACCTCTTTCACC	ATCGACGAAG		TTCTCGG M.intracellulare	
376	AAACCTCTTTCACC	ATCGACGAAG		mcmbcc M paratuberc.	
424	AAACCTCTTTCACC	ATCGACGAAG	GTCCGGGTT	TTCTAGG M.paratuberc.	
387					
389		っさいこうこうしゅう	GTCCGGGGTT	TCTCGG M. Cabereard	
528		**************	GTCCGGGTTL	TICICES M.DOVID	
			CTCH LALANA	I C CGG III TOP TO	
439		っっかつつりつつりょう	GTCCGGGGTTX	CICICGG M. Kansasza	
386			COUNTY THE HEAD OF THE	INCICES PLACE	
387					
420	AAACCTCTTTCAC	JATOGACGAAG	:cm=Ccccrr	TTCTCGG M.marinum	
381	AAACCTCTTTCAC	CATCGACGAAG	GTECGGGTT	1101000	
					
	490	500	510	520	
	490			amagang M tuberculosis	
429	ATTGACGGTAGGT	GAGAAGAAGC	ACCGGCCAA	CTACGTG M.tuberculosis	
568		. ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	'A1 1 Talat.C.AA	CIACUIO	
464					_
					=
416					
464					
424	GTTGACGGTAGGT	JGAGAAGAAG(TACCCCCAT	CTACGTG M.leprae	
479	ATTGACGGTAGGT	GGAGAAGAAG		ACTACGTG M.leprae	
426					
427					
460					
	PATCY CCCATCCA	GGAGAAGAAG	CACCGGCCA	ACTACGTG M.marinum	
421	ATIGACGGIAGGI				

Figure 5A

				
-	1130	1140	1150	1160
:	TCTCATGTTGCCAGO	GGGTAATGCC	GGGACTCGT	SAGAG M.avium
1104	TOTCATGITGCCAGG	CCCTAATGCC	GGGGACTCGT	GAGAG M.intracellulare
1056	TCTCATGTTGCCAGC	CCCTNATCC	GGGGACTCGT	GAGAG M.paratuberc.
1098	TCTCATGTTGCCAGC	GCCTAATGCC	GGGGACTCGT	GAGAG M.scrofulaceum
1064	TCTCATGTTGCCAGC	GGGTAATGCC	GGGGACTCGT	GAGAG M.tuberculosis
1069	TCTCATGTTGCCAGC	ACGTAATGGT	COCCACTOOT	GAGAG M.tuberculosis
1208	TCTCATGTTGCCAGC TCTCATGTTGCCAGC	AGGTAATGGT	GGGGACTCGT	gagag M.Dovid
1119	TCTCATGTTGCCAGC TCTCATGTTGCCAGC	AGGTAATGGT	GGGGACTCGT	GAGAG M. Teprac
1066	TCTCATGTTGCCAGC	GGGTAATGCC	:GGGGACTCGT	GAGAG M.kansasii GAGAG M.gastri
1067	TCTCATGTTGCCAGC TCTCATGTTGCCAGC	CGGGTAATGCC	GGGGACTCGT	GAGAG M.gastri
1007	mcmcn mcmmcCCAG	CGGGTAATGCC	GGGGACTCGT	GAGAG M.gordonae
1100	TOTCATGTTGCCAG	-5dcraaregr	RGGGGACTCGT	GAGAG M.marinum
1061	TCTCATGTTGCCAG	7 <u>F7</u> 0178110 <u>F</u>	_	
		-		
	1290	1300	1310	1320
			ammacan mark	EGETCT M.avium
1264	CGAATCCTTTTAAA	GCCGGACTCA	GTTCGGATIP	GGGTCT M.intracellulare
1216	CGAATCCTTTTAAA	GCCGGIICTCA	GTTCGGATTG	agamem M paratubers.
1258	CGAATCCTTTTAAA	GCCGG <u>A</u> CTCA	GTTCGGATTG	GGGTCT M.paratuberc.
1224	CGAATCCTTTTAAA	GCCGGTCTCA	GTTCGGATOG	GGGTCT M.scrofulaceum
1223	CGAATCCTTA-AAA	GCCGGTCTCA	GTTCGGATPG	GGGTCT M. Cuberculosis
1269	CGARTCCTTA-AAA	AGCCGGTCTCA	GTTCGGAT C G	GGGTCT M.scrotuldsis GGGTCT M.tuberculosis GGGTCT M.bovis GGGTCT M.leprae
1020	CCARTCCTTTTAAA	AGCCGGHCTCA	GTTCGGAT G	GGGTCT M.leprae GGGTCT M.kansasii
1226	CGARICCITI	ACCEGNATOR	GTTCGGAT	GGGTCT M.gastri
122	CGAATCCTTTAA	ACCCCCTCTCI	GTTCGGATCG	GGGTCT M.gordonae
1260	CGAATCCTTTAA	ACCCCCTCTCI	GTTCGGATCG	GGGTCT M.marinum
122	I CGAATCCTTTEMA	AGCCGGIIC I CF		GGGTCT M.marinum
	1330	1340	1350	1360
		The a grade of	NCTCCCTAGT?	ATCGCA M.avium
1304	4 GCAACTCGACCCQ	Argaag regg	AGTOGOTAGTA	AATCGCA M.intracellulare
125	6 GCAACTCGACCC	AIGAAG1000.		ARTCCCA M paratuberc.
129	8 GCAACTAGACCCA	ATGAAGTCGG:	AGTCGCTAGT	THEOCE M SCROTULACEUM
126	4 GCAACTCGACCCC	GTGAAGTCGG	AGTCGCTAGT.	AATCGCA M.scrofulaceum AATCGCA M.tuberculosis
126	8 GCAACTCGACCCC	GTGAAGTCGG	AGTCGCTAGT	AATCGCA M.tuberculosis AATCGCA M.bovis
1/10	7 CCARCTCGACCCC	GTGAAGTCGG	AGTCGCTAGT	AATCGCA M.bovis AATCGCA M.leprae
121	a GCAACTCGACCCC	GTGAAGTCGG	AGTCGCTAGT	AATCGCA M.leprae AATCGCA M.kansasii AATCGCA M.gastri
131	CONTROL CONTROL	GTGAAGTCGG	AGTCGCTAGT	AATCGCA M. Kansasii
126	S CONTINUE OF	TGAAGTCGC	AGTCGCTAGT	AATCGCA M.gastri AATCGCA M.gordonae
126	O TOTAL TOTAL CONTROL OF THE CONTROL	CTCAAGTCGC	AGTCGCTAGT	PATCGCA M.gordonae
130	O GCAACTCGACCCC	CTCAACTCCC	AGTCGCTAGT	PATCGCA M.marinum
126	50 GCAACTCGACCCC	- Para read		

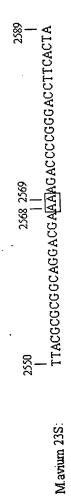


Figure 6

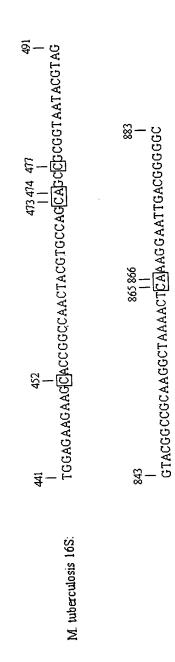


Figure 7